CLAIMS

What is Claimed Is:

1.) An isolated nucleic acid derived from a human gene encoding a protein selected from a member of the group consisting of aminopeptidase P protein (XPNPEP2), bradykinin receptor B1 protein (BDKRB1), tachykinin receptor 1 protein (TACR1), C1 esterase inhibitor protein (C1NH), kallikrein 1 protein (KLK1), bradykinin receptor B2 protein (BDKRB2), angiotension converting enzyme 2 protein (ACE2), and protease inhibitor 4 protein (PI4), wherein said nucleic acid comprises at least one polymorphic position.

2.) The isolated nucleic acid of claim 1 wherein said at least one polymorphic position for each said gene is a polymorphic position specified in Table V, or complement thereof.

3.) The isolated nucleic acid of claim 2 wherein the sequence at said at least one polymorphic position is depicted in a nucleic acid sequence selected from the group consisting of SEQ ID NO: 163 to 288; 643 to 706; and 910 to 961, and 1574 to 1575, or complement thereof.

4.) The isolated nucleic acid of claim 3 wherein said at least one polymorphic position resides in a non-coding position within the genomic sequence of said gene.

5.) The isolated nucleic acid of claim 3 wherein said at least one polymorphic position resides in a coding position within the genomic sequence of said gene.

6.) The isolated nucleic acid of claim 5 wherein said at least one polymorphic position residing in a coding position results in a missense mutation of the translated product of said gene.

7.) The isolated nucleic acid of claim 5 wherein said at least one polymorphic position residing in a coding position results in a silent mutation of the translated product of said gene.

8.) The isolated nucleic acid of claim 4 wherein said at least one polymorphic position residing in a non-coding position resides within the untranslated region of said gene.

9.) The isolated nucleic acid of claim 4 wherein said at least one polymorphic position residing in a non-coding position resides within an intronic region of said gene.

10.) The isolated nucleic acid of claim 8 wherein said at least one polymorphic position is selected from the group consisting of:

a.) 62738 of the human bradykinin receptor B2 genomic sequence;

b.) 4627 of the human kallikrein 1 genomic sequence; and

c.) 74651 of the human aminopeptidase P genomic sequence.

11.) The isolated nucleic acid of claim 10 wherein said at least one polymorphic position is selected from the group consisting of:

a.) 62738T of the human bradykinin receptor B2 genomic sequence;

b.) 62738A of the human bradykinin receptor B2 genomic sequence;

c.) 4627C of the human kallikrein 1 genomic sequence;

d.) 4627T of the human kallikrein 1 genomic sequence;

e.) 74651C of the human aminopeptidase P genomic sequence; and

f.) 74651T of the human aminopeptidase P genomic sequence.

12.) The isolated nucleic acid molecule according to claim 11, wherein asid nucleic acid sequence is at least 30 nucleotides in length.

13.) The isolated nucleic acid molecule according to claim 11, wherein said nucleic acid sequence is at least 40 nucleotides in length.

14.) A probe that hybridizes to a polymorphic position defined in claim 2.

15.) The probe of claim 14 wherein said probe is at least 15 nucleotides in length.

16.) The probe of claim 15 wherein a central position of the probe aligns with said polymorphic position.

17.) The probe of claim 15 wherein the 3' end of the primer aligns with said polymorphic position.

18.) A method of analyzing at least one nucleic acid sample, comprising the steps of (1) obtaining said nucleic acid sample from one or more individuals; and (2) determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group consisting of aminopeptidase P protein (XPNPEP2), bradykinin receptor B1 protein (BDKRB1), tachykinin receptor 1 protein (TACR1), C1 esterase inhibitor protein (C1NH), kallikrein 1 protein (KLK1), bradykinin receptor B2 protein (BDKRB2), angiotension converting enzyme 2 protein (ACE2), and protease inhibitor 4 protein (PI4).

19.) The method according to claim 18, further comprising the steps of (3) testing each individual for the presence of a disease phenotype; and (4) correlating the presence of the disease phenotype with the sequence at said one or more polymorphic positions.

20.) The method according to claim 19, wherein said one or more polymorphic position of said nucleic acid sequence is a polymorphic position specified in Table V for said gene.

21.) The method according to claim 20, wherein the nucleic acid sequence at said one or more polymorphic position is depicted in a nucleic acid sequence selected from the group consisting of SEQ ID NO:163 to 288; 643 to 706; and 910 to 961, and 1574 to 1575, or complement thereof.

22.) A method of constructing haplotypes using the isolated nucleic acids of claim 1, comprising the step of grouping at least two said nucleic acids.

23.) The method according to claim 22 further comprising the step of using said haplotypes to identify an individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with said haplotype.

24.) The method according to claim 19 further comprising the step of quantifying the nucleic acid sample comprising the polymorphic base.

25) The method according to claim 21 or 23 wherein the disease phenotype is angioedema or an angioedema-like disorder.

26) The method according to claim 25 wherein the polymorphic position is a member of the group consisting of:

a.) 62738 of the human bradykinin receptor B2 genomic sequence;

b.) 4627 of the human kallikrein 1 genomic sequence; and

c.) 74651 of the human aminopeptidase P genomic sequence.

27) The isolated nucleic acid of claim 26 wherein the sequence at the polymorphic position is a member of the group consisting of:

a.) 62738T of the human bradykinin receptor B2 genomic sequence;

b.) 62738A of the human bradykinin receptor B2 genomic sequence;

c.) 4627C of the human kallikrein 1 genomic sequence;

d.) 4627T of the human kallikrein 1 genomic sequence;

e.) 74651C of the human aminopeptidase P genomic sequence; and

f.) 74651T of the human aminopeptidase P genomic sequence.

28) A method for identifying an individual at risk of developing a disorder upon administration of a pharmaceutically acceptable amount of an ACE inhibitor and/or vasopeptidase inhibitor comprising the steps of

a.) obtaining nucleic acid sample(s) from said individual;

b.) amplifying one or more sequences from said sample(s) using appropriate PCR primers for amplifying across at least one polymorphic position;

c.) comparing said at least one polymorphic position with a known data set; and

d.) determining whether the result correlates with an increased or decreased risk for developing a disorder.

29) The method according to claim 28 wherein said at least one polymorphic position is selected from the group consisting of:

a.) 62738 of the human bradykinin receptor B2 genomic sequence;

b.) 4627 of the human kallikrein 1 genomic sequence; and

c.) 74651 of the human aminopeptidase P genomic sequence.

30) The isolated nucleic acid of claim 29 wherein said at least one polymorphic position is selected from the group consisting of:

a.) 62738T of the human bradykinin receptor B2 genomic sequence;

b.) 62738A of the human bradykinin receptor B2 genomic sequence;

c.) 4627C of the human kallikrein 1 genomic sequence;

d.) 4627T of the human kallikrein 1 genomic sequence;

e.) 74651C of the human aminopeptidase P genomic sequence; and

f.) 74651T of the human aminopeptidase P genomic sequence.

31) The method of claim 30 wherein the disorder is angioedema or an angioedema-like disorder.

32) A library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group consisting of aminopeptidase P protein (XPNPEP2), bradykinin receptor B1 protein (BDKRB1), tachykinin receptor 1 protein (TACR1), C1 esterase inhibitor protein (C1NH), kallikrein 1 protein (KLK1), bradykinin receptor B2 protein (BDKRB2), angiotension converting enzyme 2 protein (ACE2), and protease inhibitor 4 protein (PI4), wherein said polymorphic positions are selected from a group consisting of the polymorphic positions provided in Table V.

33) The library of nucleic acids of claim 32 wherein the sequence at said polymorphic position is selected from the group consisting of the sequences provided in Table V.

34) The library according to claim 33 wherein the polymorphic position is a member of the group consisting of:

a.) 62738 of the human bradykinin receptor B2 genomic sequence;

b.) 4627 of the human kallikrein 1 genomic sequence; and

c.) 74651 of the human aminopeptidase P genomic sequence.

35) The library according to claim 34 wherein the sequence at the polymorphic position is a member of the group consisting of:

a.) 62738T of the human bradykinin receptor B2 genomic sequence;

b.) 62738A of the human bradykinin receptor B2 genomic sequence;

c.) 4627C of the human kallikrein 1 genomic sequence;

d.) 4627T of the human kallikrein 1 genomic sequence;

e.) 74651C of the human aminopeptidase P genomic sequence; and

f.) 74651T of the human aminopeptidase P genomic sequence.

36) The library according to claim 35 wherein said library of isolated sequences represents the complimentary sequence of said sequences.

37) A kit for identifying an individual at risk of developing a disorder upon administration of a pharmaceutically acceptable amount of an ACE inhibitor and/or vasopeptidase inhibitor, said kit comprising

i.) sequencing primers, and

ii.) sequencing reagents,

wherein said primers are primers that hybridize to at least one polymorphic position in a human gene selected from the group consisting of aminopeptidase P protein (XPNPEP2), bradykinin

receptor B1 protein (BDKRB1), tachykinin receptor 1 protein (TACR1), C1 esterase inhibitor protein (C1NH), kallikrein 1 protein (KLK1), bradykinin receptor B2 protein (BDKRB2), angiotension converting enzyme 2 protein (ACE2), and protease inhibitor 4 protein (PI4).

38) The kit according to claim 37 wherein said polymorphic positions are selected from a group consisting of the polymorphic positions provided in Table V.

39) The kit according to claim 38 wherein the polymorphic position is a member of the group consisting of:

a.) 62738 of the human bradykinin receptor B2 genomic sequence;

b.) 4627 of the human kallikrein 1 genomic sequence; and

c.) 74651 of the human aminopeptidase P genomic sequence.

40) The kit according to claim 39 wherein the sequence at the polymorphic position is a member of the group consisting of:

a.) 62738T of the human bradykinin receptor B2 genomic sequence;

b.) 62738A of the human bradykinin receptor B2 genomic sequence;

c.) 4627C of the human kallikrein 1 genomic sequence;

d.) 4627T of the human kallikrein 1 genomic sequence;

e.) 74651C of the human aminopeptidase P genomic sequence; and

f.) 74651T of the human aminopeptidase P genomic sequence.

41) The kit according to claim 40 wherein said primer(s) hybridizes immediately adjacent to said polymorphic positions.

42) The kit according to claim 41 wherein said primer(s) hybridizes to said polymorphic positions such that the central position of the primer aligns with the polymorphic position of said gene.

43) The method according to claim 28 further comprising the step of subjecting the product(s) of said amplification to a genetic bit analysis (GBA) reaction.

44) A method for identifying an individual at risk of developing a disorder upon administration of a pharmaceutically acceptable amount of an ACE inhibitor and/or vasopeptidase inhibitor comprising the steps of

a.) obtaining a nucleic acid sample(s) from said individual;

b.) determining the nucleotide present at least one polymorphic position,

c.) comparing said at least one polymorphic position with a known data set; and

d.) determining whether the result correlates with an increased or decreased risk for developing a disorder.

45) The method according to claim 44 wherein said at least one polymorphic position is selected from the group consisting of:

a.) 62738 of the human bradykinin receptor B2 genomic sequence;

b.) 4627 of the human kallikrein 1 genomic sequence; and

c.) 74651 of the human aminopeptidase P genomic sequence.

46) The isolated nucleic acid of claim 45 wherein said at least one polymorphic position is selected from the group consisting of:

a.) 62738T of the human bradykinin receptor B2 genomic sequence;

b.) 62738A of the human bradykinin receptor B2 genomic sequence;

c.) 4627C of the human kallikrein 1 genomic sequence;

d.) 4627T of the human kallikrein 1 genomic sequence;

e.) 74651C of the human aminopeptidase P genomic sequence; and

f.) 74651T of the human aminopeptidase P genomic sequence.

47) The method of claim 46 wherein the disorder is angioedema or an angioedema-like disorder.

48) A method for genotyping an individual comprising the steps of

a.) obtaining a nucleic acid sample(s) from said individual;

b.) determining the nucleotide present at least one polymorphic position, and

c.) comparing said at least one polymorphic position with a known data set.

49) The method according to claim 48 wherein said at least one polymorphic position is selected from the group consisting of:

a.) 62738 of the human bradykinin receptor B2 genomic sequence;

b.) 4627 of the human kallikrein 1 genomic sequence; and

c.) 74651 of the human aminopeptidase P genomic sequence.

50) The isolated nucleic acid of claim 49 wherein said at least one polymorphic position is selected from the group consisting of:

a.) 62738T of the human bradykinin receptor B2 genomic sequence;

b.) 62738A of the human bradykinin receptor B2 genomic sequence;

c.) 4627C of the human kallikrein 1 genomic sequence;

d.) 4627T of the human kallikrein 1 genomic sequence;

e.) 74651C of the human aminopeptidase P genomic sequence; and

f.) 74651T of the human aminopeptidase P genomic sequence.